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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:17:03 ; Search time 2461.04 seconds

(Without alignments)  
10930.628 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661

Sequence: 1 GAATCGGCTCATATGCA.....TGGCGGATAGCCGATTC 1661

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 809743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthum:\*  
16: em\_estom:\*  
17: gb\_ges8:\*  
18: em\_ges8\_hum:\*  
19: em\_ges8\_inv:\*  
20: em\_ges8\_pln:\*  
21: em\_ges8\_vit:\*  
22: em\_ges8\_fun:\*  
23: em\_ges8\_mam:\*  
24: em\_ges8\_mus:\*  
25: em\_ges8\_other:\*  
26: em\_ges8\_pro:\*  
27: em\_ges8\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	28.4	2265	11	AY109623
2	431.4	26.0	2290	11	AY104969
3	430.6	25.9	2338	11	AY103778
4	414.2	24.9	1327	17	BH770613
5	383.6	23.1	2143	11	AY108560
6	302.8	18.2	1376	11	AY106465

7	290	17.5	1387	11	AY108518
8	263.2	15.8	887	17	CNS0740M
9	262.8	15.8	1090	14	BW799922
10	261.8	15.8	878	12	BE275584
11	257.2	15.5	1035	9	AL518632
12	254	15.3	977	12	BC321293
13	253.4	15.3	988	9	AL532233
14	251.6	15.1	955	9	AL515562
15	249.6	15.0	1017	9	AL515579
16	249	15.0	810	12	BF627437
17	248.6	15.0	810	12	BF627437
18	248	14.9	959	9	AL557150
19	247	14.9	746	14	BH003474
20	246.4	14.8	980	9	AL557181
21	245	14.8	765	14	BO867621
22	243	14.6	645	10	AM224051
23	242	14.6	633	14	BH014013
24	239.4	14.4	718	14	DA6006
25	237.6	14.3	637	10	AM223768
26	237.6	14.3	1119	13	BM458421
27	236.2	14.2	668	10	AM398404
28	233	14.0	771	12	BF617440
29	231.2	13.9	677	10	AV938920
30	230.2	13.9	698	14	BO860576
31	229.6	13.8	1051	13	BM478208
32	228.8	13.8	744	14	BU000648
33	227.4	13.7	680	10	AM330455
34	227.2	13.7	632	12	BG128308
35	226.6	13.6	650	9	AC432272
36	226	13.6	790	12	BC599254
37	226	13.6	1351	10	BE422296
38	225.6	13.6	895	14	BO216655
39	225.4	13.6	946	14	BO882339
40	225.2	13.6	709	9	AT486676
41	224.8	13.5	1016	13	BM450130
42	224.8	13.5	739	14	BO915279
43	223	13.4	744	13	BI176450
44	222.4	13.4	654	13	BI176456
45	222.4	13.4	825	10	BE642158

## ALIGNMENTS

RESULT 1  
AY109623  
LOCUS 2265 bp mRNA linear HTC 25-MAY-2002  
DEFINITION Zea mays CL2221\_1 mRNA sequence.  
ACCESSION AY109623  
VERSION AY109623.1 GI:21213414  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 2265)  
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitfield, M.S.,  
Arthur, L.M., Hainey, M., Morgan, M. and Finney, S.V.  
Maize Mapping Project/DuPont Consensus Sequences for Design of  
Overgo Probes (2002)  
Unpublished (2002)  
CoE, E.C.  
Direct Submission  
Submitted (25-APR-2002) Maize Mapping Project, University of  
Missouri, Columbia, MO 65211, USA  
Location/Qualifiers  
1. 2265  
/organism="Zea mays"  
/db\_xref="MaizeDB:630867"  
/db\_xref="taxon:4577"  
/clone="CL2221\_1"

/clone\_1lb="Maize Mapping Project/DuPont Consensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"

BASE COUNT 615 a 430 c 599 g 538 t 83 others  
 Query Match 28.4% Score 472; DB 11; Length 2265;  
 Best Local Similarity 55.4%; Pred. No 1,3e-120;  
 Matches 913; Conservative 0; Mismatches 697; Indels 9; Gaps 3;

OY 13 ATATGCAAAAGAAATTCATTTACAGATCCGCTGCTCCATGTCGCGGAGTTG 72  
 DB 288 ATGCTGGAGACATCAAGTTGGTGTGAGGCCGCTCTGTATNNNNNNNNNN 347  
 OY 73 ATATGTTAGCAGATACGCTCAAAAGTAAAGCTTGGTCTTAAAGGGGCAATGTTGTTG 132  
 DB 348 NNN 407  
 OY 133 AAAAAGCTTTGTTCCCTTAATTAATGACGGGGTACCAATGCTAAAGACATG 192  
 DB 408 AGCAAAAGCTTTGTTCCCTTAATTAATGACGGGGTACCAATGCTAAAGACATG 467  
 OY 193 AATTAGAGATCATTTGAAAACATGGAGCAAAATTTGTTCTGAAGTGGCTTAA 232  
 DB 468 AATTAGAGATCATTTGAAAACATGGAGCAAAATTTGTTCTGAAGTGGCTTAA 527  
 OY 253 CCATGATATTTCTGATGATGGAGACTACTGACACTTTTACACAGCCATGTC 312  
 DB 528 CTATATGACCTCTGGGATGATGACCAATGTCCTTTTACAAAGCAATTTA 567  
 OY 313 ATGAGGACTATAAATATGACAGAGTGTATCAATTTGATTCCTGACAGCATG 372  
 DB 588 CTGAGGGGTCATTAATGTTGGGATGATGATGATGATGATGATGATGATGAT 647  
 OY 313 AAACAGACAGCAACAGCTGTGAAGCTTGAAGCCATTTGCTCAACTGTATCTGCA 432  
 DB 648 CAATGCTCTTACGCTGTGTGACCAATGTAAGAGGAGGAGGAGGAGGAGGAG 707  
 OY 433 AGNAGCTATTTGCTAGTGGTGCAGATATCACTGCTGAAA--AAGTTGAGAGT 489  
 DB 708 CAGAGAAATTTGACAGAGTGGTACATATCAGCAAAATGGGAAAGGAAATTTGGTGC 767  
 OY 490 ATATCTCAGAGCTATGAGCGTGTGGCAAGAGTGTGTATTCATTCAGAGATCTC 549  
 DB 768 TTAATCTCCAGAGCTATGAGAGGAGTGGCAAAAGGAGGAGTGTATTCAGAGG 827  
 OY 550 GAGGTATGAAAAGACATTTGAAGTGGTGAAGGACATTTGACCGTGTACCTT 609  
 DB 828 ACACCTTTATATAGAGCTTGAAGTGGTGAAGGATTTGAATCTGACAGAGTTTACCT 887  
 OY 610 CTCATATACATGCTGACAGCAATGAAAATGTTGACAGCTTGAAGAACCTTTATCT 669  
 DB 888 CTCGATCTATTTACCACTGCAAGAGCCAGAAATGTAATGTAAGGAGGAGGAGGAG 947  
 OY 670 TAAATCAGATATAAAGTGTCAAAATCCAGACATTTTCCACTTGTGAGAGAGTTC 729  
 DB 948 TAAATCAGATATAAAGTGTCAAAATCCAGACATTTTCCACTTGTGAGAGAGTTC 1007  
 OY 730 TTAAGCAACCGTCAATTTACTATTTACATGATGATGATGATGATGATGATGAT 789  
 DB 1008 TGAAGAACAAAGAGCTTACTGATGATGATGATGATGATGATGATGATGATGAT 1067  
 OY 790 CCCTTGTCTGAGAGATTTGCTGATTTCAAGTGGTGTGCTGCTGCAAGGCGCAGAGT 849  
 DB 1068 CTTTGTATTTATCAAGCTTGTGAGGATCAAGTGTGCTGCTGCAAGGCGCAGAGT 1127  
 OY 850 TTGCTGATGCTGCTGAAGCTATGCTGAAGATGCTATCTTCAAGAGTGTGCTGATGA 909

DB 1128 TTGGGAAAACAGAGAACCAACTTACAGAGCTTGCATCTTACTGAGAGAGGTAA 1187  
 OY 910 TTACAGAGATCTAGAGACTTGAATTAAGATCTACATACAGCCCTGGACAGCTG 969  
 DB 1188 TAACTGAGAACATGAGATGAACTTGAATTTGACCTGACATGCTGGGTACATGCA 1247  
 OY 970 CTAAATATACATGTTGATTAAGTATGACACATTAATTTGATGAGAGTTCAGAG 1029  
 DB 1248 NNNNGTACATGCTCTTAAGATGACATGTTATTTCTTGAAGAGGCGGAGCAAGAGT 1307  
 OY 1030 CTATTTGCTAACCGTATTTGCTATGATTAATTCGCAATTTAGAACACACTTGTCT 1089  
 DB 1308 CATTTGAAGAGAGGAGGAGAGATTTAGATGACATTTGAGAAATACATCTTCAATTA 1367  
 OY 1090 ACCGTGAAAACACTCAAGAGAGTGTGGCAAAATTTAGCTGAGTGTAGCTGTATCAAG 1149  
 DB 1368 ATAAAGAAAAGCTCCAGAGGAGGTTGGCAAAAGCTCTGTGAGGTTGTCTTGAAGA 1427  
 OY 1150 TAGGAGCTCCACAGAGAGAGCTTTAAAGAAATGAAATTCGATGAGAGTGGCTCTTA 1209  
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 DB 1488 ATGTACATGAGCTGCTGTGAGAGAGGATTTGACAGAGGAGGAGGAGGAGGAGG 1547  
 OY 1270 CGGTATTTGAAAAGTACAGAGCTTTGAGCTG--AGGCGATGATGCTAGAGAGTA 1326  
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 OY 1327 ACATTTGCTTCTGCTCTAGAGAGAGCTGTACGTAATTTGATTTAACTGCTGGTAC 1386  
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 OY 1387 AAGGCTCCGATGATTTGACAG--TTGAAAACAGCCCTGAGAGAGAGATTTAA 1443  
 DB 1668 AGGAGAGAGAGATGATGAGAGAGCTTTTGGACAGAAATTTACTGCTGGGTATGAG 1727  
 OY 1444 CTGCAAGAGGTGAGGCTGATGATTAATTAACAGAGATCATGAGCTGCTCAAGTA 1503  
 DB 1728 CTGCTAAAGGTGATGATTTGATGATGATGATGATGATGATGATGATGATGAT 1787  
 OY 1504 CAGCATGAGGCTTCAAAATGAGCTGTGATGATGATGATGATGATGATGATGATGAT 1563  
 DB 1788 TCAGAGACTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1847  
 OY 1564 TTGTTGCTAATAACCTGACAGAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGG 1622  
 DB 1848 TAAATTTAGAGATTTCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1906

RESULT 2  
 AV104969 2290 bp mRNA Linear HTC 25-MAY-2002  
 LOCUS AV104969  
 DEFINITION 2ea mays PC0070942 mRNA sequence.  
 ACCESSION AV104969  
 VERSION AV104969.1 GI:21208047  
 KEYWORDS HTC.  
 SOURCE 2ea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 2250)  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.W., Hainey, M., Morgan, M., and Tinsley, S.V.  
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 2250)  
 AUTHORS Coe, E.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA  
Location/Qualifiers  
1 2290  
/organism="Zea mays"  
/db\_xref="MaizeDB:633867"  
/db\_xref="taxon:457"  
/clone="PC0070942"  
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/note="This sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 684 a 457 c 583 g 565 t 1 others

Query Match 26.08; Score 431.4; DB 11; Length 2290;  
Best Local Similarity 57.98; Pred No 3.1e-109;  
Matches 883; Conservative 0; Mismatches 622; Indels 19; Gaps 6;

QY 66 GGAGTGTATCTTACAGATACCGTCAAGTAAACGCTTGTCTTAAGGGCGCAATGTT 125  
DB 426 GGGGTCAACAGCTTGTGACATCTGCGGGGTTACTCTTGACCAAGGGCGCAATGTA 485  
QY 126 GTTCTTAAAAAGCTTTGGTCTCCCTTAATTAATGATGAGGGGTAAACCATTTGTTAA 185  
DB 486 GTCTCGAAGAGATGATGCTCACTAAATGTCAATGATGCTGCTGCGCAAG 545  
QY 186 GAGATCGAATTAAGATCATTTGAAACATGSGAGCAAAATGGTGTGAAGTGGT 245  
DB 546 GAGGTGAATGAGAGACCGCTTGAATTAATGCTTAATGCTCCGCAAGCTGCT 605  
QY 246 TCTAAACATGATATGCTGGTGAATGGAGAGCTGCTCAACAGTTTGAACAGAGC 305  
DB 606 GCTAAACAAATGACTGCTGGTGAATGGAGAGCACTGCTGCTGCTCAAGG 665  
QY 306 ATGTGTCAAGAGACTAAAAAATGTGACAGCAGCTGCTTAATCAATGATGATCCTGA 365  
DB 666 ATGATTAAGAGAGCTTAAGAGTGTGAGTGTGCTGCTTAATCAATGATGATCCTGA 725  
QY 366 GGCATTGAAGAGCAAGCAAGAGCTGTGAACCTTTGAAGCCATTGCTCAACTGTA 425  
DB 726 GGTATTGAAAGAGCAAGCAAGAGCTGTGAACCTTTGAAGCCATTGCTCAACTGTA 785  
QY 426 TCTGGCAAGAGCTATTTGCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482  
DB 786 TGAGGAGAGTGAAG--TTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843  
QY 483 GGAGAGTATATCTCAGAGATGATGAGAGCTGTGGGAGAGATGATGATGATGATGAT 542  
DB 844 GGGATATATGATGCTGAGGCTATGAAAGAGTGGGAGAGAGAGTGGTGCACACTTGA 903  
QY 543 GAATCTGAGATGATGAAACAGAACTTGAAGTGTGAAAGGATGATGATGATGATGAT 602  
DB 904 GAAGGAAAGAGTGTGAAATTAACCTGATTTGTTGTTGTTGTTGTTGTTGTTGTTG 963  
QY 603 TACCTGCTCAATGATGCTGACAGCAAGCAATGAAATGTTGCAAGCTTTGAAGCA 662  
DB 964 TATATTTCTCCCTACTTGTGCTGACAGTGAAGAAAGAGTGTGAGTGTGAGATTTGC 1023  
QY 663 TTTATCTTAATCAGGATAAAAAGTGTCAAAATCAACATGATTTTGGCCTACTGTAG 722  
DB 1024 AAGCTTCTCTGTGAGCAAGAAATTAACAAATGACAGATCTTATCACTATCTGAG 1083  
QY 723 GAAGTCTTAAACCAAGCTCCATTAATTAATGATGATGATGATGATGATGATGATGAT 782  
DB 1084 GATGCTATTAGAGTGTGATTCATTTAATGATGATGATGATGATGATGATGATGAT 1143  
QY 783 CTTCACACCTTGTCTTGAACAAAGATGATGATGATGATGATGATGATGATGATGAT 842  
DB 1144 CTTCACACCTTGTGATTAATGCTTGAAGTGTGATGATGATGATGATGATGATGATGAT 1203

QY 843 CCAGATTTGTGATGCTGCTAAAGCTATGCTTGAAGATGCTATCTTACAGAGTGT 902  
DB 1204 CTTGTTTGGAGGAGCCCAAAAGTCAATATCTGATGATGATGATGATGATGATGATGAT 1263  
QY 903 ACAGTATTACAGAGATCTAGAGCTTGAATTAAGATGCTTGAAGATGATGATGATGATGAT 962  
DB 1264 ACTGCTATCAGAGAGAGAGTGTGATTAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1323  
QY 963 CAGGCTGATGATTAATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1022  
DB 1324 ACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383  
QY 1023 TCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1082  
DB 1384 CAG 1443  
QY 1083 GACTTGACCGTGAAGAACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1142  
DB 1444 GAATATGAG 1503  
QY 1143 ATCAAGTATGAG 1202  
DB 1504 ATTCAGATGAG 1563  
QY 1203 GCTCTAAATGCTTACAG 1262  
DB 1564 GCGCTAAATGCTTACAG 1623  
QY 1263 CTATATGAGGTTATGAAAG 1316  
DB 1624 CTTTGTAGGCTTGTATGAAAG 1683  
QY 1317 AC---TGGAGCTAATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373  
DB 1684 AAGGTTGGGCTGAAAG 1743  
QY 1374 AATGCTGGGCTGAAAG 1429  
DB 1744 AATGCAAGGCTTAAATGAG 1803  
QY 1430 AACAGATTTAATGCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1489  
DB 1804 TATGGG-TTCAATGCGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1862  
QY 1490 CCCTGCTCAAGTAAACAGATCAGGCTTCAAAATGCTGCTGCTGCTGCTGCTGCTGCTG 1549  
DB 1863 TCCACCAAGAGGTTGTAGAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1922  
QY 1550 GACACAG 1573  
DB 1923 CACCTGTATGAG 1946

RESULT 3  
LOCUS AY103778 2338 bp mRNA linear HTC 25-MAY-2002  
DEFINITION Zea mays PC0063180 mRNA sequence.  
ACCESSION AY103778  
VERSION AY103778.1 GI:21206856  
KEYWORDS HTC.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whittle M.S.,  
Arthur L.W., Hanafey M., Morgante M. and Tingey S.V.  
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of  
Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 2338)

QY	785	TCACACCCCTGCTCTTGAACAACATTCGTCGCTACTTTCATTAAGTGGTTCGTCGCAACAGCCG	844
Db	1172	TGCACCCCTTGCTCCTCAACACACTCAGAGGATCTAGAAAGTCCGTCACATCAAAAAGCCG	1231
QY	845	AGAAATTTGGTATGCTGCTAAAGCATGATGCTTGAAGCACTTGTATCTTGACAGGTGTAC	904
Db	1232	TGGTTTGTGAGAGCCAAACACACAGTACTTGGATATATGCAATCTTACTGAGGACAC	1291
QY	905	AGGATTTACAGAGATCTTAGACTTGAATTAAGAAGTCTACATGACAGCCCTTGAGACA	964
Db	1292	TGTATACAGATATGAGTTGGGCTGTCACTGTGCAAGGCTGACAAATTCAGTTCTTGGAAC	1351
QY	965	GCGTCTTAAGTTACAGTTGATTAAGATACACACTAATTTGTTGAAGTTGACGAAGTTTC	1024
Db	1352	AGCTGGAAAGGTTGTCTCTTACGAAAGAGTGCACAACTATGTTGGTGTGACACACCCA	1411
QY	1025	AGAGCTATTGCTACCGTATGTCACGTATTAATGCAATTTGAAATGAAACAACTCTGA	1084
Db	1412	GGAAGAAATTTCTTAAGAGGGTTGACAGATTAATAATCTATTAAGACGACGACACAA	1471
QY	1085	CTTTCACCGTAAACAACTACAGAACCTTTGGCGAAATTAAGCTGTGGTGTAGCTGTAT	1144
Db	1472	ATTGAAAGGAAAAAAGCTCAATGAGAGATATACCAAGCTTGCTGGTGGTGTGTGTAT	1531
QY	1145	CAAGCTAGAGACCTCCAAAGAGACAGCTTAAAGAAATTAACCTGCAATGAGATGC	1204
Db	1532	TCAGTGGGAGACCAACAGAACTGACCTAAAGAAAGAAAGTTAAAGTTAGAGATGC	1591
QY	1205	TCTAATGCTACAGCTGCAGCGCTGTAAGAGATGCTGCTGCTGTGGTGGAAACAGACT	1264
Db	1592	CCTAATGCTCAACCAAGGCTGCTTTGAGGAAGATTTGTTGTTGGTGGAGATGCAACCT	1651
QY	1265	TATTAAGGTTATTAAGAAAGTAGACACTTGTACCT-----GAGGCGATGATGC	1315
Db	1652	TTTGGCGCTTGCAAGCTAAAGTCATGTCATCAAGATTAACGTGAGAACTGATGACAGA	1711
QY	1316	TACGTGACGTAAATTTGCTTGTGCTGTAGAAAGCCTGTAGCTCAAAATGCTTTAA	1375
Db	1712	GCTTGAGCTGAATATGTAAGAGGCGCTGAGCTACCCCTTAATATGTTCTTAAAA	1771
QY	1376	TGCTGGCTACGAAGGCTCCGATGATTTAGCAAGTTGAAAAACAGCCCTGCAGGA	1432
Db	1772	TGCGCGGTCAATGACAGCTGCTACGTACAGACAGTGAAGAGTCTTTTAAAGATTACTCA	1831
QY	1433	AGGATTTATGCTGCAACAGGTAGTGGTGTGATGATTAACAGAGATCAATTTAGCC	1492
Db	1832	TGTTTAAACATGCTGCTACTGACAGACAGTGAAGATTTGAGGCTGTGATTCATTTGATCC	1891
QY	1493	TGCTAAGTAAACAGCATCAGCGCTTAAATAAGTACAGCTCTGTAGTATGATTTTAAAC	1552
Db	1892	TGCTAAGTGTGTAAGATCTGTTGTGAGCATGCGCGGTGGGCAAGACCTTCCTGAC	1951
QY	1553	AACAGAAAGCAGTTGCTGCTAATAACCTGAAACAGCTAGACCCAGGCGACACATGCG	1609
Db	1952	ATGCTAGTGTGGTGGTGTGCTGATTAATTAAGAGCCAGAGTGTGGCCCTTGTCTAACC	2008
RESULT 4			
LOCUS	BH770613/c	1327 bp	DNA linear
DEFINITION	LMWG49372 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic DNA sequence.		
ACCESSION	BH770613		
VERSION	BH770613.1	GI:20373570	
KEYWORDS	GSS		
SOURCE	Lactococcus lactis subsp. cremoris.		
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.		
REFERENCE	1 (bases 1 to 1327)		
AUTHORS	Bolotin,A., Ehrlich,S.D. and Sorokin,A.		
TITLE	Studies of genomes of dairy bacteria Lactococcus lactis		
JOURNAL	Sci. Aliments, (2002) In press		

Wed Apr 16 08:05:37 2003

us-09-001-737-7.rst

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COMMENT

Contact: Sorokin A  
Genetique Microbiome

INRA

CRU INRA, Domaine de Villvert, 78152 Jouy en Josas cedex, France

Tel: 33 1 34 65 25 16

Fax: 33 1 34 65 25 21

Email: sorokine@jouy.inra.fr

Best homologue in strain IL1403 is groEL (93%)

Class: Shotgun

High quality sequence start: 30

High quality sequence stop: 1299.

Location/Qualifiers

1. 1327

/organism="Lactococcus lactis subsp. cremoris"

/strain="MG1363"

/db\_xref="taxon:1359"

/clone\_lib="MG1363 Random Sequence Tag Library"

/note="Vector: pSGM2; Site 1: Small: Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

BASE COUNT 392 a 292 c 239 g 403 t 1 others

ORIGIN

Query Match 24.9%; Score 414.2; DB 17; Length 1327;

Best Local Similarity 72.0%; Pred. No. 1.4e-104;

Matches 553; Conservative 0; Mismatches 214; Indels 1; Gaps 1;

830 TGCTGCAAGCCGAGGATTTGGTGTCTGTAAGCTATGCTTGAAGACATTCCTAT 889

1322 TGCTGTAAGACCGGATTTGGTGTCTGTAAGCTATGCTTGAAGACATTCCTAT 1264

890 CTTCAGAGTGTGTACAGTGTATACAGAGATCTGAGACTTGAATTAAGATCTCAAT 949

1263 CTTCAGAGTGTGTACAGTGTATACAGAGATCTGAGACTTGAATTAAGATCTCAAT 1204

950 GACAGCCCTTGAAGAGCTGTCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1009

1203 AGAAGCTTTAGACAGAGCTGTCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1144

1010 AGGTTCAGAGTGTGTACAGTGTATACAGAGATCTGAGACTTGAATTAAGATCTCAAT 1069

1143 AGGTTCAGAGTGTGTACAGTGTATACAGAGATCTGAGACTTGAATTAAGATCTCAAT 1084

1070 AACAACTCTGTGACTTGTACAGTGTATACAGAGATCTGAGACTTGAATTAAGATCTCAAT 1129

1083 AAAAATACCTGTGTATTTGCTGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1024

1130 TGGTGAGCTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1189

1023 CGGAGTGTGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 964

1190 TCGCATTTGAGATGTCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1249

963 TTTGATTTGAAGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 904

1250 TGTGTGAGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1309

903 TGTGTGAGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 844

1310 TGATGCTAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1369

843 CATCAACAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 784

1370 TTTAATGCTGTGTGAGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1429

783 GGCATGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 724

1430 AACAGATTTAAGTGTGAGAGTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1489

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Db 603 GACTACTGAGAGTGTGCTGCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 556

RESULT 5

AY108560

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

1 (bases 1 to 2143)

1 (bases 1 to 2143)

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittle, M.S.,

Arthur, L.W., Hanley, M., Morgan, M., and Tingey, S.V.

Maize Mapping Project/Dupont Consensus Sequences for Design of

Overgo Probes

Unpublished (2002)

2 (bases 1 to 2143)

Co/E.C.

Direct Submission

Submitted (25-Apr-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

Location/Qualifiers

1. 2143

/organism="Zea mays"

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Library"

/note="This sequence is part of a project of EST

assemblies resulting from the application of public

contigs to seed Dupont contigs; this resource was

assembled by Dupont as part of a collaboration for the

overgo addressing of BACs in conjunction with the Maize

Mapping Project"

BASE COUNT 546 a 494 c 598 g 505 t

ORIGIN

Query Match 23.1%; Score 383.6; DB 11; Length 2143;

Best Local Similarity 54.0%; Pred. No. 7.5e-96;

Matches 880; Conservative 0; Mismatches 734; Indels 16; Gaps 4;

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334 CTCGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 393

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 SOURCE Zea mays.  
 ORGANISM Zea mays.  
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 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 1376)  
 Hainey, C.E., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 Unpublished (2002)  
 2 (bases 1 to 1376)  
 Coe, E.C.  
 Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
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 contigs to seed Dupont contigs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACS in conjunction with the Maize  
 Mapping Project."  
 BASE COUNT 397 a 277 c 359 g 343 t  
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658 ACCATTATCTTAATCAGGATTAAGTGTCAACATCCAAACATTTTCCACTAC 717  
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 VERSION AY108518.1 GI:21211596  
 KEYWORDS HTC.

SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1387)  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,  
 Arthur, L.W., Hainey, M., Morgante, M., and Tingey, S.V.  
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 1387)  
 AUTHORS Coe, E.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
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BASE COUNT 426 a 257 c 372 g 332 t  
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 748 TGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
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D <sub>b</sub>	6 25	TTTATTACCAGCCCTTAATCTGTAAGGAGGAAATTTGAAAACCTTTGATCTTATTAGGT	684
O <sub>Y</sub>	6 78	GATATAAAAGTGCACAACTCCAGACATTTTGGCACTACTACTGAGAAAGTTCTTAAAC	737
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DEFINITION	BM799922	AGSCNOUTT.6417164 NIH_MGC_67 Homo sapiens	CDNA clone IMAGE:5492101		
ACCESSION	BM799922	5' mRNA sequence.			
VERSION	BM799922.1	GI:19116745			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Ekmanlyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1090)  
NIH-NCBI <http://img.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strassberg Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLNL12113 row: x column: 14  
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ORIGIN				

Query Match	Score	DB ID	Length
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Best local similarity	56.24		
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Matches 514; Conservative 0; Mismatches 397; Indels 3; Gaps 1

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Db 182 TTACCGCATGCTGTGGCCGTACAAATGGGGCCAAAGGAAACAGTCATTTATTCAGCAG 241

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Db		422	GGCTTCGAGAAAGATTAGCAAAGGTCCTAATCCATGCAAAATCAGAGAGGGTGATGTTH	481
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Db		482	GGCTGTGATGGTGTATTAATTGCTGAAACTTAAAGACAGTCTAAACCTGTACACCCTGTAA	541
Oy		438	GCTATTGCTCAGGTGCTGCGCATATCACGCGCTCTGAAAAG--TTGAGAGATATATC	494
Db		542	GAAATTTGACACAGGTTGTCTACAGATTTCTGCAAAACGAGACAAAGAAATTTGCCAATATCATC	601
Oy		495	TGAGAGCTATGAGAGCGTGTGGCAACGATGGTGATTTACCATCGAAGATCTGAGGT	554
Db		602	TCTGATGCATATGAAAAAGTTGGAGAAAGGGTGCTCATCACGATGAAGATGAAAAACA	661
Oy		555	ATGGAACACAACTGGAAGTGGTTGGAAGCATCATCAATTGGACCGGTTCCTGTCTCA	614
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Db		842	CACGTAAGCCTTTGGCTATATTCGCTGAAGATGTATGATGAGAAAGCTCTACATGATCACTC	901
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Db		902	GCTTTGATTAATGGCTAAAGGTGGCTCTCCAGGGGTGGCAGTCACAGCTCAGGGGTTTTGT	961
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ACCESSION	Bf273584			
VERSION	Bf273584.1			
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SOURCE	Gossypium arboreum.			
ORGANISM	Gossypium arboreum			
REFERENCE	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Rosidae; eudicots II; Malvales; Malvaceae; core eudicots;			
TITLE	Ming,R.A., Fisch.D., Yu.Y., Main,D., Rambo,T., Simmons,J., Henry			
JOURNAL	'D., Wood,T.C., Leslie,A. and Wilkins,T.A.			
	An integrated analysis of the genetics, development, and evolution			
	of the cotton fiber			
	Unpublished (2000)			

RESULT 10	
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DEFINITION	BF275584 878 bp mRNA linear EST OF MAR-2001
ACCESSION	GA_EB0024G23f Gossypium arboreum 7-10 dpa fiber library gossypium
VERSION	BF275584 cDNA clone GA_EB0024G23f, mRNA sequence.
KEYWORDS	BF275584.1 GI:1120654
SOURCE	EST.
ORGANISM	Gossypium arboreum. Gossypium arboreum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; eucotylids II; Malvales; Malvaceae; Gossypium. I (bases 1 to 878)
REFERENCE	Ming, R.A., Fischel, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
JOURNAL	Unpublished (2000)

	COMMENT	Contact: Ming RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel.: 864 656 7288 Fax: 864 656 4293 Email: rlvine@clemson.edu Seq primer: TTAATGCACTCATTAAGGG High quality sequence stop: 716. location/Qualifiers
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Db	Best Local Similarity	58.1%; Pred. No. 6e-62;
	Matches 458; Conservative	0; Mismatches 330; Indels 0; Gaps 0
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Oy	541 AAGATCTCGAGTATGSAAGACAACTGGAAGTGTGAAGGCATGATTTACCCTG 600	
Db	88 AGCATCATCTCTATTTGAGCCACAGTTGATGTGGAGAAGATGGAGATTACAGG 147	
Oy	601 GTTACCTGCTCATATCATGTCTCACAGACANTGAAGAAATGGTGCAGACCTTAAAC 660	
Db	148 GTTACATCTCCCACATTTGTATATAACCCGGAGAAATGGTGTGAGTTTGAAAG 207	
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Oy	781 CACTTCCACCCCTTGTCTTGACAGAGATCTGTGTACTTCAATGTGGTCTCTGAAG 840	
Db	328 CTCTGCCACACCTGTGGTGAACAAACGCGCTGCATTCCTAAATGTGCACCAATTAAG 387	
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Db	388 CTCCTGTGTTTTGTGAAAGGAAAAGCTCTTCCTTCAMAGATTTGCCATTCGACTGGTG 447	
Oy	901 GTACAGTATTAAGAGAGATCTAGAGACTTGGATTAAGATGCTACAAATGACACCCCTTG 960	
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Oy	961 GACAGGCTGCTAGATTAACATTTGATTAAGATPACACATTAATTTGGTAGTACAGGAA 1020	
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Oy	1021 GTTACAGAGTATTTGCTAACGTTATTCGACATGATTAATCCGATTTGAAGAAACACACT 1080	
Db	568 CAAGAGTATGATTCANMCTGAGGGTGGCAACATTAAGAAAGAGCTAGCTCAGACAGATT 627	
Oy	1081 GTACTTTGACCCTGAAAAATCAAGACCTTTGGCGAAATTTAGTGGTGTGTACTG 1140	
Db	628 CTGTCTATGATTCAGAAAAATTTGGCAGAAAGATGGCCAAACTCTCTGGTGGTGTTCAG 687	
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Db 688 TCATTAAAGTGGGGGCTGCACAGAGAGACTGACATGACATCTGACCTACGATTAG 747
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Oy 1261 CACTATT 1268
Db 808 CCTTGT 815

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DEFINITION AL518632 LTI_NFL011.NBC1 Homo sapiens cDNA clone CS0DA009y115
prime, mRNA sequence.
ACCESSION AL518632
VERSION AL518632.1 GI:12782125
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Poljans, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91005 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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organism="Homo sapiens"
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clone="CS0DA009y115"
gene="LTI_NFL011.NBC1"
sex="male"
tissue="neuroblastoma cells"
lab="host=DM10B"
note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@life-tech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 311 a 195 c 259 g 266 t 4 others
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Best Local Similarity 56.3%; Pred. No. 1.3e-60;
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Oy 138 GCTTTTGCTTCCTTAATTACTAATAGCGGGTACCATCTGCTAAAGATGCAATG 197
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Db 356 GAAAGAGCTGGGATGACACTACACTGCTCTACTGACGCGCTCTATAGCAAGAA 415
OY 318 GGACTAAAAATGTCACAGAGCTGCTATTCATTTGATTCCTGAGAGCATGAAACA 377
Db 416 GGCTTGAGAGATTAACAAAGGCTGCTATTCACATGGAATACGAGAGAGTGTATTA 475
OY 378 GCAACAGCAACAGCTGTTGAAGCCTTGAAGCCATTGCTCAACCTGATCTGCAAGAA 437
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OY 438 GCTATTGCTCAGAGTCTGCTGAGTATCATCAGCTCTGAAAAAG---TTGAGAGTATTC 494
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OY 495 TCAGAAAGCTATGAGAGCTGTGGGCAACGATGCTGATTAACATCGAAGAACTCGAGGT 554
Db 596 TCTGATGCAATGAAAAAGTTGAGAGAAAGGCTGTCTACACAGTAAAGATGAGAAACA 655
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Db 656 CTGAATGATGAAATTAAGAAATTAATTAAGAGAGCTGCTGCTGCTTAAATTTCTCCA 715
OY 615 TACATGCTCAGACAAATGAAAAATGTTGACAGCTTGAAGAACCCATTTATCTTAATC 674
Db 716 TACTTATTAATACATTAAGAGTCAAGAAATGTAATTCAGAGATGCTTGTCTGTG 775
OY 675 ACGATTAATAAAAGTTCACAAATCCAAACATTTTCCACTACTGAGAGATTTTAAA 734
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ACCESSION BG31293
VERSION BG31293.1 GI:13150971
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Panic
clade: Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 977)
Singh, J.A., Makul, K., Courroux, P., De Moors, A., Harris, L.J., Hattori,
J.I., Ouellet, T., Robert, L.S., Sprout, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings
Unpublished (2001).
COMMENT
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neely Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.

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FEATURES
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Best Local Similarity 56.7%; Pred. No. 9.8e-60;
Matches 440; Conservative 23; Mismatches 310; Indels 3; Gaps 1;

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OY 67 GAGTGAATATGTAGACATACCGTCAAGTACGCTGCTCCTTAAGGGCGCATGTTG 126
Db 262 GTGTTGAGAGAGTTGGCAGAGMCGCTTAAGATTACAAATGAGCTAAGGCGCATGTTG 321
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Db 322 TTATTGAGCAACCTTTGCTGCAACCAAGTACAAAGATGCTGTTTGAACAAAGA 381
OY 187 AGATGAAATTAAGATCATTTTGAAGACAGAGCAAAATTTGCTGTAAGTGGCTT 246
Db 382 GCATTGAATTAAGATAGATTAAGAAAGTGGTGAACACCTTGAACAGGTTGTA 441
OY 247 CTAAACCAATGATATTCCTGCTGATGAGACACTACTGCACAGTTTGAACAGCA 306
Db 442 ATGCMCTAATGACACTTCTGCGATGATGACCATATKCACTTTTGAACAAAGCA 501
OY 307 TTGTCATGAGAGACTTAAAAATGTGACAGAGTGTCTAATCAATTTGATTCCTGAG 366
Db 502 TATTACTGAGGAGTGCAAAATCTGTCGCGCTGAATKATGCTATGGATTTAAGCGCTG 561
OY 367 GCATTGAACAGCAACAGCAACAGCTGTGAAGCCTTGAAGACCAATTCCTCACTGAT 426
Db 562 GAAACTCAATGCTGTTGAGCGCTGTTTACCAATCTTAAGATGAGCCAGATATATCA 621
OY 427 CTGCGAAGAGAGTATTCCTCAGTCCGTCGAGTATGATCAGCGCTGAAA---AAGTTG 483
Db 622 GCATTCAGAGAAATTCACAGAGTGGTGTGATCAATATACGAATATGGGAAAGGAATTG 681
OY 484 GAGAGTAAATTCACAGAGCTATGACAGCTGTGGCAACGATGCTGATTAACATGAG 543
Db 682 GTGAGCTATGTCAGAGCTATGAGAGAGTGTGCAAGAGGCTTTAAMCATTTGCGG 741
OY 544 AATCTCAGAGTATGCAAGACAACTGAAGTGTGAAGCATGCAATTTGACCGTGT 603
Db 742 ACGTAAACACCCCTTATATAGACTTAAAGTGTGAGGATTTAACTGACAGAGRTT 801
OY 604 ACTGTCTAATATCATATGCTCAGACAGCAATGAAGAAATGTTGTCAGACCTGAAACCAT 663
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OY 664 TTATCTTAATCAGGATTAAGAAAGTGTCAACATCAAGCAATTTGGCACTACTTGAAG 723
Db 862 TGATCTTAATATCATACAGAGAGTGTGACAGATCATCTCTGCTTAAGCTTTAGAA 921
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DEFINITION	AL532233 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSDB00041YR20 5				
ACCESSION	AL532233				
VERSION	AL532233.1	GI:12795726			
KEYWORDS	EST.				
ORGANISM	human				
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JOURNAL					
COMMENT					
FEATURES					
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BASE COUNT	306 a 188 c 242 g 251 t				1 others
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Matches 500; Conservative	0; Mismatches 371; Indels 4; Gaps 2;				
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OY	138 GCTTTTGGTCTCCCTTAATTACTATGACGCGGTAAACCATTCGTAAGAGATTA 197				
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Db	355 GAAAGACTTGGGATGAGTCACTACCACTGCTACTGTACTGACGCTGTATGACCAAGAA 414				
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Db	415 GGCTTCGAGAGATTTGCAAAAGGTGTATTCATGAGTGAAGAGAGGTGTATGTTA 474				
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VERSION	AL515262.1		
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SOURCE	human		
ORGANISM	Homo sapiens		
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AUTHORS	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers		
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BASE COUNT	288 a	181 c	236 g
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Med Apr 16 08:05:37 2003

us-09-001-737-7.rst

Page 13

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Best Local Similarity 57.0%; Pred. No. 4.6e-59;  
Matches 480; Conservative 0; Mismatches 359; Indels 3; Gaps 1;

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PRIMER, mRNA sequence.  
ACCESSION AL515579

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

human.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1017)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 9106 Evry cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

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/lab="Most-DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@life.com  
http://fulllength.invitrogen.com"

BASE COUNT 308 a 191 c 255 g 261 t 2 others

ORIGIN

Query Match 15.0%; Score 249.6; DB 9; Length 1017;  
Best Local Similarity 56.8%; Pred. No. 1.7e-38;  
Matches 478; Conservative 1; Mismatches 360; Indels 3; Gaps 1;

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78 TTACAGATACCGTCAAGATGAGCTTGGTCTTAAGGGCGCAATGTTCTTGA 137  
176 TTAGCGGATGCTGTGGCGCTGTACAAATGGGCGCAAGAGAGATGATTAAGCAG 235  
138 GCTTTGGTTCCTTAAATTAATGAGGGGATCAATCTGTAAGAGATGAATTA 197  
236 AGTTGGGAATGCCAAGATTAACAAGATGGTGTGATGTCAGAAAGTCAATGACTTA 295  
198 GAAGATCAATTTGAAAGCATGGGAGCAAAATTTGGTGTGTAAGTGGCTTCAAAACCAT 257  
296 AAGATTAATCAAAAACATTTGAGCTTAATCTGTAAGTGTGTAAGTGGCTTCAAAACCAT 355  
258 GATATGCTGTGATGAGGAGCAGCTATGCAACAGTTTGAACACCATTTGCTATGA 317  
356 GAAGAGCTGGGATGGACACACAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 415  
318 GCACTAAAAAATGTGACAGAGGTGTAATCCAAATGATTCCTGAGAGCATGAAACA 377  
416 GCGTTCGAGAGATTAAGAGGTGTAATCCAGATGAGAGAGAGGTGATGATTA 475  
378 GCAACAGCAACAGCTTTGAGAGCTTGAAGCATTTGCTCAACCTGATCTGCAAGAA 437  
476 GCGTGTGATGCTGTATTTGCTGAATCAAAAAAGCAGCTTCAACCTGATGACCCCTGAA 535  
438 GCTATGCTAGGCTGCTGATATCATCAGCTTGAAGAAAG--TTGAGAGATATATC 494  
536 GAATTTGCAAGAGTTGCTACGATTTTGCACAAAGGAGCAAGAAATTTGGCAATATCATC 595

